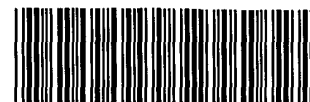


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DATE: 02/12/2002

PATENT APPLICATION: US/09/987,107

TIME: 15:32:09

Input Set : A:\GRAVERSEN1A.txt

Output Set: N:\CRF3\02122002\I987107.raw

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3 <110> APPLICANT: GRAVERSEN, Jonas
4   MOESTRUP, Soren
6 <120> TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
8 <130> FILE REFERENCE: GRAVERSEN1A
10 <140> CURRENT APPLICATION NUMBER: US 09/987,107
11 <141> CURRENT FILING DATE: 2001-11-13
13 <150> PRIOR APPLICATION NUMBER: US 60/264,022
14 <151> PRIOR FILING DATE: 2001-01-26
16 <150> PRIOR APPLICATION NUMBER: DK PA2001 00057
17 <151> PRIOR FILING DATE: 2001-01-15
19 <150> PRIOR APPLICATION NUMBER: DK PA2000 01682
20 <151> PRIOR FILING DATE: 2000-11-10
22 <160> NUMBER OF SEQ ID NOS: 91
24 <170> SOFTWARE: PatentIn version 3.1
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27 <211> LENGTH: 243
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
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37 Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln
38                20                    25                    30
41 Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp
42                35                    40                    45
45 Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu
46                50                    55                    60
49 Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu
50 65                    70                    75                    80
53 Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys
54                85                    90                    95
57 Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met
58                100                   105                   110
61 Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu
62                115                   120                   125
65 Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu
66                130                   135                   140
69 Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg
70 145                   150                   155                   160
73 Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala
74                165                   170                   175
77 Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr
78                180                   185                   190

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81 His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys
82 195 200 205
85 Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser
86 210 215 220
89 Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu
90 225 230 235 240
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99 <212> TYPE: PRT
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105 <223> OTHER INFORMATION: N-terminal Cys
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110 <222> LOCATION: (2)..(244)
111 <223> OTHER INFORMATION: Amino acids 25-267 from human ApoA1
114 <400> SEQUENCE: 2
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117 1 5 10 15
120 Thr Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser
121 20 25 30
124 Gln Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu
125 35 40 45
128 Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln
129 50 55 60
132 Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr
133 65 70 75 80
136 Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala
137 85 90 95
140 Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu
141 100 105 110
144 Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln
145 115 120 125
148 Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro
149 130 135 140
152 Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu
153 145 150 155 160
156 Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala
157 165 170 175
160 Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu
161 180 185 190
164 Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala
165 195 200 205
168 Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu
169 210 215 220
172 Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys

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188 <223> OTHER INFORMATION: Trimerisation module from tetranectin
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192 <221> NAME/KEY: misc_feature
193 <222> LOCATION: (59)..(301)
194 <223> OTHER INFORMATION: Mature ApoA1
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203 Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
204          20          25          30
207 Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
208          35          40          45
211 Ala Leu Gln Thr Val Ser Leu Lys Gly Ser Asp Glu Pro Pro Gln Ser
212          50          55          60
215 Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu
216 65          70          75          80
219 Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu
220          85          90          95
223 Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr
224          100         105         110
227 Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu
228          115         120         125
231 Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met
232          130         135         140
235 Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp
236 145         150         155         160
239 Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys
240          165         170         175
243 Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu
244          180         185         190
247 His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp
248          195         200         205
251 Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr
252          210         215         220
255 Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys
256 225         230         235         240
259 Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu
260          245         250         255
263 His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu
264          260         265         270

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267 Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu
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272       290           295           300
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277 <212> TYPE: PRT
278 <213> ORGANISM: Homo sapiens
280 <220> FEATURE:
281 <221> NAME/KEY: misc_feature
282 <222> LOCATION: (1)..(58)
283 <223> OTHER INFORMATION: Trimerisation module from tetranectin
286 <220> FEATURE:
287 <221> NAME/KEY: misc_feature
288 <222> LOCATION: (59)..(258)
289 <223> OTHER INFORMATION: Amion acids 68-267 from human Apo A1
292 <400> SEQUENCE: 4
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298 Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
299           20           25           30
302 Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
303       35           40           45
306 Ala Leu Gln Thr Val Ser Leu Lys Gly Ser Leu Lys Leu Leu Asp Asn
307       50           55           60
310 Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly
311 65           70           75           80
314 Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly
315           85           90           95
318 Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val
319           100          105          110
322 Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu
323       115          120          125
326 Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly
327       130          135          140
330 Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly
331 145          150          155          160
334 Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr
335           165          170          175
338 His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg
339           180          185          190
342 Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His
343       195          200          205
346 Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro
347       210          215          220
350 Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe
351 225          230          235          240
354 Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn
355           245          250          255

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Output Set: N:\CRF3\02122002\I987107.raw

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358 Thr Gln
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363 <211> LENGTH: 301
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365 <213> ORGANISM: Homo sapiens
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370 <223> OTHER INFORMATION: Trimerisation module from tetranectin
373 <220> FEATURE:
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375 <222> LOCATION: (9)..(9)
376 <223> OTHER INFORMATION: Mutagen
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382 <223> OTHER INFORMATION: Mutagen
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387 <222> LOCATION: (59)..(301)
388 <223> OTHER INFORMATION: Apo-A1 mature
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397 Ala Lys Ala Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
398 20 25 30
401 Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
402 35 40 45
405 Ala Leu Gln Thr Val Ser Leu Lys Gly Ser Asp Glu Pro Pro Gln Ser
406 50 55 60
409 Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu
410 65 70 75 80
413 Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu
414 85 90 95
417 Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr
418 100 105 110
421 Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu
422 115 120 125
425 Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met
426 130 135 140
429 Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp
430 145 150 155 160
433 Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys
434 165 170 175
437 Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu
438 180 185 190
441 His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp
442 195 200 205
445 Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr

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VERIFICATION SUMMARY

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